

## IN THE CLAIMS

Claims 1, 130, 138-140, and 143-145 have been amended. New claims 151 and 152 have been added. Claims 1, 60, 61, 130, 133, 138-140, 143-145, 151 and 152 are pending in the instant application. The following is the status of the claims of the above-captioned application, as amended.

1. (Currently Amended) A ~~microbial variant~~ of a trypsin ~~polypeptide variant having chymotrypsin-like activity~~, comprising the specific combination of modifications as follows:

- (a) substitutions at positions corresponding to positions 144, 193, 198, 201, 218, 223, 227, 228, 229, 230, and 231 of amino acids 25 to 248 of SEQ ID NO: 2;
- (b) deletions at positions corresponding to positions 192, 197, and 226 of amino acids 25 to 248 of SEQ ID NO: 2; and
- (c) an insertion between positions corresponding to positions 224 and 225 of amino acids 25 to 248 of SEQ ID NO: 2;

wherein the variant of the trypsin polypeptide has chymotrypsin activity; the ~~microbial~~ trypsin polypeptide is (a) a polypeptide comprising an amino acid sequence which has at least 90% identity to amino acids 25 to 248 of SEQ ID NO: 2; or (b) a polypeptide encoded by a nucleotide sequence which hybridizes under at least medium-high stringency conditions with nucleotides 202 to 801 of SEQ ID NO: 1 or its complementary strand, wherein medium-high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and 35% formamide followed by washing three times each for 15 minutes using 2X SSC, 0.2% SDS at 60°C; and the variant comprises an amino acid sequence that has at least 90% identity to amino acids 25 to 248 of SEQ ID NO: 2 of the trypsin polypeptide.

2-59. (Cancelled).

60. (Original) The variant of claim 1, which is encoded by the nucleotide sequence contained in pEJG66.1XLGOLD which is contained in *E. coli* NRRL B-30627.

61. (Previously Presented) The variant of claim 1, which is in a form of a precursor comprising amino acids 1 to 24 of SEQ ID NO: 2 as a prepro region, or a portion thereof, linked in translation reading frame with the amino terminus of the trypsin variant.

62-129. (Cancelled).

130. (Currently Amended) A laundry detergent composition comprising the variant of claim 1 and a surfactant.

131. (Cancelled).

132. (Cancelled).

133. (Previously Presented) The variant of claim 1, which comprises the substitutions V144T + S193A + D198S + Q201M + A218I + N223S + R227S + P228T + N229S + Y230T + S231P, the deletions V192\* + K197\* + A226\*, and the insertion G224GT of amino acids 25 to 248 of SEQ ID NO: 2.

134. (Cancelled).

135. (Cancelled).

136. (Cancelled).

137. (Cancelled).

138. (Currently Amended) The variant of claim 1, wherein the ~~microbial~~ trypsin polypeptide has an amino acid sequence which has at least 90% identity ~~with~~ to amino acids 25 to 248 of SEQ ID NO: 2.

139. (Currently Amended) The variant of claim 138, wherein the ~~microbial~~ trypsin polypeptide has an amino acid sequence which has at least 95% identity ~~with~~ to amino acids 25 to 248 of SEQ ID NO: 2.

140. (Currently Amended) The variant of claim 1, wherein the ~~microbial~~ trypsin polypeptide has the amino acid sequence of amino acids 25 to 248 of SEQ ID NO: 2.

141. (Cancelled).

142. (Cancelled).

143. (Currently Amended) The variant of claim 1, wherein the ~~microbial~~ trypsin polypeptide is encoded by a nucleotide sequence which hybridizes under medium-high stringency conditions with nucleotides 202 to 801 of SEQ ID NO: 1 or the nucleotide sequence of nucleotides 202 to 801 of SEQ ID NO: 1, wherein medium-high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and 35% formamide followed by washing three times each for 15 minutes using 2X SSC, 0.2% SDS at 60°C.

144. (Currently Amended) The variant of claim 143, wherein the ~~microbial~~ trypsin polypeptide is encoded by a nucleotide sequence which hybridizes under high stringency conditions with nucleotides 202 to 801 of SEQ ID NO: 1 or the nucleotide sequence of nucleotides 202 to 801 of SEQ ID NO: 1, wherein high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and 50% formamide followed by washing three times each for 15 minutes using 2X SSC, 0.2% SDS at 65°C.

145. (Currently Amended) The variant of claim 1, wherein the ~~microbial~~ trypsin polypeptide is a wild-type ~~microbial~~ trypsin polypeptide.

146-151. (Cancelled).

151. (New) The variant of claim 139, wherein the trypsin polypeptide has an amino acid sequence which has at least 97% identity to amino acids 25 to 248 of SEQ ID NO: 2.

152. (New) The variant of claim 1, which comprises amino acids 25 to 246 of SEQ ID NO: 4..